# NiceProt View of Swiss-Prot: Q64280

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

*Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.*

**Entry information**

| | |
|---|---|
| Entry name | **TGF4_MOUSE** |
| Primary accession number | **Q64280** |
| Secondary accession numbers | None |
| Entered in Swiss-Prot in | Release 35, November 1997 |
| Sequence was last modified in | Release 35, November 1997 |
| Annotations were last modified in | Release 44, July 2004 |

**Name and origin of the protein**

| | |
|---|---|
| Protein name | **Transforming growth factor beta 4 [Precursor]** |
| Synonyms | **TGF-beta 4**<br>**Lefty protein**<br>**Lefty-1 protein**<br>**STRA3 protein** |
| Gene name | **Name: Ebaf**<br>Synonyms: Tgfb4, Stra3, Lefty, Lefty1 |
| From | Mus musculus (Mouse) [TaxID: 10090] |
| Taxonomy | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |

**References**

[1] SEQUENCE FROM NUCLEIC ACID.
DOI=10.1038/381151a0;MEDLINE=96202359;PubMed=8610011 [NCBI, ExPASy, EBI, Israel, Japan]
Meno C., Saijoh Y., Fujii H., Ikeda M., Yokoyama T., Yokoyama M., Toyoda Y., Hamada H.;
"Left-right asymmetric expression of the TGF beta-family member lefty in mouse embryos.";
Nature 381:151-155(1996).

[2] SEQUENCE FROM NUCLEIC ACID.
Bouillet P.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE FROM NUCLEIC ACID.

# NiceProt View of Swiss-Prot: O00292



## Entry information

| | |
|---|---|
| Entry name | **TGF4_HUMAN** |
| Primary accession number | **O00292** |
| Secondary accession numbers | O75611 Q8NBQ9 |
| Entered in Swiss-Prot in | Release 35, November 1997 |
| Sequence was last modified in | Release 40, October 2001 |
| Annotations were last modified in | Release 44, July 2004 |

## Name and origin of the protein

| | |
|---|---|
| Protein name | **Transforming growth factor beta 4 [Precursor]** |
| Synonyms | **TGF-beta 4**<br>**Endometrial bleeding-associated factor**<br>**Left-right determination factor A**<br>**Lefty-A protein** |
| Gene name | **Name: EBAF**<br>Synonyms: TGFB4, LEFTA, LEFTYA |
| From | Homo sapiens (Human) [TaxID: 9606] |
| Taxonomy | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |

LEFTY-B
LEFTB
LEFN1
LEFTY2
LEFTY A

## References

[1] SEQUENCE FROM NUCLEIC ACID.
**TISSUE**=Placenta;
MEDLINE=97298127;PubMed=9153275 [NCBI, ExPASy, EBI, Israel, Japan]
Kothapalli R., Buyuksal I., Wu S.-Q., Chegini N., Tabibzadeh S.;
"Detection of ebaf, a novel human gene of the transforming growth factor beta superfamily association of gene expression with endometrial bleeding.";
J. Clin. Invest. 99:2342-2350(1997).

[2] REVISIONS.
MEDLINE=99162193;PubMed=10053005 [NCBI, ExPASy, EBI, Israel, Japan]
Kothapalli R.;
Unpublished results, cited by: Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,

Casey B.; Am. J. Hum. Genet. 64:712-721(1999).

[3] SEQUENCE FROM NUCLEIC ACID, AND VARIANT L-R AXIS MALFORMATIONS ASN-342.
**TISSUE**=Placenta;
MEDLINE=99162193;PubMed=10053005 [NCBI, ExPASy, EBI, Israel, Japan]
Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G., Casey B.;
"Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left-right axis development.";
Am. J. Hum. Genet. 64:712-721(1999).

[4] SEQUENCE FROM NUCLEIC ACID.
DOI=10.1038/ng1285;PubMed=14702039 [NCBI, ExPASy, EBI, Israel, Japan]
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
"Complete sequencing and characterization of 21,243 full-length human cDNAs.";
Nat. Genet. 36:40-45(2004).

[5] SEQUENCE FROM NUCLEIC ACID.
**TISSUE**=Ovary;
DOI=10.1073/pnas.242603899;MEDLINE=22388257;PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA

sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

**Comments**

- ***FUNCTION***: Required for left-right (L-R) asymmetry determination of organ systems in mammals. May play a role in endometrial bleeding.
- ***SUBCELLULAR LOCATION***: Secreted.
- ***TISSUE SPECIFICITY***: Mesenchymal cells of the endometrial stroma.
- ***DEVELOPMENTAL STAGE***: Transiently expressed before and during menstrual bleeding.
- ***PTM***: The processing of the protein may also occur at the second R-X-X-R site located at AA 132-135. Processing appears to be regulated in a cell-type specific manner.
- ***DISEASE***: Defects in EBAF are the cause of left-right axis malformations (L-R axis malformation) [MIM:601877]. The defect includes left pulmonary isomerism, with cardiac anomalies characterized by complete atrioventricular canal defect and hypoplastic left ventricle, and interrupted inferior vena cava.
- ***SIMILARITY***: Belongs to the TGF-beta family.

**Copyright**



**Cross-references**

| | |
|---|---|
| EMBL | U81523; AAB53269.1; ALT_SEQ. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF081511; AAC32600.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF081508; AAC32600.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF081509; AAC32600.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF081510; AAC32600.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF081513; AAD48145.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>AK075344; BAC11556.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>BC035718; AAH35718.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| HSSP | P10600; 1TGJ. [HSSP ENTRY / PDB] |
| Genew | HGNC:3122; EBAF. |
| CleanEx | HGNC:3122; EBAF. |
| GeneCards | EBAF. |
| GeneLynx | EBAF; Homo sapiens. |
| GenAtlas | EBAF. |
| MIM | 601877 [NCBI / EBI]. |
| GO | GO:0007275; Biological process: development *(traceable author statement).*<br>GO:0007309; Biological process: oocyte axis determination *(traceable author statement).*<br>GO:0007179; Biological process: transforming growth factor beta receptor signaling pathway *(traceable author statement).*<br>QuickGo view. |
| SOURCE | EBAF; Homo sapiens. |
| Ensembl | O00292; Homo sapiens. [Entry / Contig view] |
| InterPro | IPR001839; TGFb.<br>IPR001111; TGFb_N.<br>Graphical view of domain structure. |

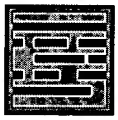
| | |
|---|---|
| Pfam | PF00688; TGFb_propeptide; 1.<br>PF00019; TGF_beta; 1.<br>Pfam graphical view of domain structure. |
| ProDom | PD000357; TGFb; 1.<br>[Domain structure / List of seq. sharing at least 1 domain] |
| PROSITE | PS00250; TGF_BETA_1; 1. |
| HOVERGEN | [Family / Alignment / Tree] |
| BLOCKS | O00292. |
| ProtoNet | O00292. |
| ProtoMap | O00292. |
| PRESAGE | O00292. |
| DIP | O00292. |
| ModBase | O00292. |
| SMR | O00292; 63A416CAE30F7A39. |
| SWISS-2DPAGE | Get region on 2D PAGE. |
| UniRef | View cluster of proteins with at least 50% / 90% identity. |

**Keywords**

**Cytokine**; **Developmental protein**; **Disease mutation**; **Glycoprotein**; **Growth factor**; **Multigene family**; **Signal**.

**Features**

 Feature table viewer

 Feature aligner

| Key | From | To | Length | Description | FTId |
|---|---|---|---|---|---|
| SIGNAL | 1 | 21 | 21 | *Potential.* | |
| PROPEP | 22 | 76 | 55 | Or 135 (*Potential*). | |
| CHAIN | 77 | 366 | 290 | Transforming growth factor beta 4. | |
| DISULFID | 251 | 264 | | *By similarity.* | |
| DISULFID | 263 | 316 | | *By similarity.* | |
| DISULFID | 293 | 351 | | *By similarity.* | |
| DISULFID | 297 | 353 | | *By similarity.* | |
| CARBOHYD | 158 | 158 | | N-linked (GlcNAc...) (*Potential*). | |
| VARIANT | 342 | 342 | * | S -> N (in L-R axis malformations). | VAR_010385 |
| CONFLICT | 183 | 183 | | A -> P (in Ref. 4). | |

**Sequence information**

Length: **366 AA** [This is the length of the unprocessed precursor]

Molecular weight: **40920 Da** [This is the MW of the unprocessed precursor]

CRC64: **63A416CAE30F7A39** [This is a checksum on the sequence]

```
         10         20         30         40         50         60
          |          |          |          |          |          |
MWPLWLCWAL WVLPLAGPGA ALTEEQLLGS LLRQLQLSEV PVLDRADMEK LVIPAHVRAQ

         70         80         90        100        110        120
          |          |          |          |          |          |
YVVLLRRSHG DRSRGKRFSQ SFREVAGRFL ASEASTHLLV FGMEQRLPPN SELVQAVLRL
```

```
     130         140         150         160         170         180
      |           |           |           |           |           |
FQEPVPKAAL HRHGRLSPRS AQARVTVEWL RVRDDGSNRT SLIDSRLVSV HESGWKAFDV

     190         200         210         220         230         240
      |           |           |           |           |           |
TEAVNFWQQL SRPRQPLLLQ VSVQREHLGP LASGAHKLVR FASQGAPAGL GEPQLELHTL

     250         260         270         280         290         300
      |           |           |           |           |           |
DLRDYGAQGD CDPEAPMTEG TRCCRQEMYI DLQGMKWAKN WVLEPPGFLA YECVGTCQQP

     310         320         330         340         350         360
      |           |           |           |           |           |
PEALAFNWPF LGPRQCIASE TASLPMIVSI KEGGRTRPQV VSLPNMRVQK CSCASDGALV
```

PRRLQP

O00292 in FASTA format

*View entry in original Swiss-Prot format*
*View entry in raw text format (no links)*
*Report form for errors/updates in this Swiss-Prot entry*

**BLAST** BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

ExPASy Home page | Site Map | Search ExPASy | Contact us | Swiss-Prot

Hosted by NCSC US | Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan

# Search in Swiss-Prot and TrEMBL for: tgfb4

## Swiss-Prot Release 44.5 of 13-Sep-2004
## TrEMBL Release 27.5 of 13-Sep-2004

---

- Number of sequences found in Swiss-Prot$_{(2)}$ and TrEMBL$_{(0)}$: **2**
- For more directed searches, you can use the Sequence Retrieval System SRS.

---

### Search in Swiss-Prot: There are matches to 2 out of 158316 entries

TGF4_HUMAN (**O00292**)
Transforming growth factor beta 4 precursor (TGF-beta 4) (Endometrial bleeding-associated factor) (Left-right determination factor A) (Lefty-A protein). {GENE: Name=EBAF; Synonyms=TGFB4, LEFTA, LEFTYA} - Homo sapiens (Human)

TGF4_MOUSE (**Q64280**)
Transforming growth factor beta 4 precursor (TGF-beta 4) (Lefty protein) (Lefty-1 protein) (STRA3 protein). {GENE: Name=Ebaf; Synonyms=Tgfb4, Stra3, Lefty, Lefty1} - Mus musculus (Mouse)

---

### Search in TrEMBL: There are matches to 0 out of 1400820 entries

---

New Search

in Swiss-Prot/TrEMBL by AC, ID, description, gene name, organism

**Please do NOT use any boolean operators (and, or, etc.)**

**7/3,KWIC/5 (Item 1 from file: 399)**
DIALOG(R)File 399:CA SEARCH(R)


**111091468 CA: 111(11)91468h JOURNAL**
**Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid encoding transforming growth factor .beta. 4 from chicken embryo chondrocytes**
AUTHOR(S): Jakowlew, Sonia B.; Dillard, Pamela J.; Sporn, Michael B.; Roberts, Anita B.
LOCATION: Lab. Chemoprev., Natl. Cancer Inst., Bethesda, MD, 20892, USA
JOURNAL: Mol. Endocrinol. DATE: 1988 VOLUME: 2 NUMBER: 12 PAGES: 1186-95 CODEN: MOENEN ISSN: 0888-8809 LANGUAGE: English
? t s17/9/3 4

**17/9/3 (Item 1 from file: 73)**
DIALOG(R)File 73:EMBASE


06240683 EMBASE No: 1995269574
**The immunomodulatory diversity of the proteins of the transforming growth factor beta (TGFbetaP) family**
Wieczorek Z.; Sion J.; Kluczyk A.; Zbozien R.; Stafanowicz P.; Siemion I.Z.
L. Hirschfeld Inst Immun/Exp Therapy, Polish Academy of Sciences, Czerska 12,53-114 Wroclaw Poland
International Journal of Peptide and Protein Research ( INT. J. PEPT. PROTEIN RES. ) (Denmark) 1995, 46/2 (113-118)
CODEN: IJPPC ISSN: 0367-8377
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The examination of immunomodulatory properties of oligopeptides derived from two exposed loops (containing thymopentin-like and tuftsin-like sequences, respectively) of the proteins belonging to TGFbeta family suggests that the particular species of the TGFbeta family should differ distinctly in their influence on the immune response. According to our results obtained from three TGFbeta species of mammals, TGFbeta 2 should be a strong immunosuppressor, whereas for TGFbeta 3 the immunostimulative potency is more probable. TGFbeta 1 species would possess both immunosuppressive and immunostimulative potency, residing in two different loops of the protein. The results obtained also suggest that chicken **TGFbeta4** should be associated with immunostimulative effects and xenopus TGFbeta5 with immunosuppressive ones.

DRUG DESCRIPTORS:
*transforming growth factor beta--pharmacology--pd; *transforming growth factor beta--drug comparison--cm; *transforming growth factor beta--drug analysis--an; *transforming growth factor beta--drug development--dv
thymopentin--drug comparison--cm
MEDICAL DESCRIPTORS:
*delayed hypersensitivity; *immunomodulation
animal experiment; article; controlled study; drug purification; drug synthesis; high performance liquid chromatography; mouse; nonhuman; protein variant
CAS REGISTRY NO.: 69558-55-0 (thymopentin)
SECTION HEADINGS:
026 Immunology, Serology and Transplantation
029 Clinical and Experimental Biochemistry
030 Clinical and Experimental Pharmacology

**17/9/4 (Item 2 from file: 73)**


06190248 EMBASE No: 1995227311

**Expression of transforming growth factor beta in the embryonic avian lens coincides with the presence of mitochondria**

Potts J.D.; Bassnett S.; Beebe D.C.
Department of Anatomy/Cell Biology, Uniformed Svcs. Univ. of Health Sci., 4301 Jones Bridge Road,Bethesda, MD 20814-4799 United States

Developmental Dynamics ( DEV. DYN. ) (United States) 1995, 203/3 (317-323)
CODEN: DEDYE ISSN: 1058-8388
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

During their maturation, lens cells lose all membrane bound organelles, including mitochondria. In chicken embryos this process begins in the central lens fibers beginning around embryonic day 12 (E12). Transforming growth factor beta (TGFbeta) is a multipotent growth modulator thought to play a role in numerous developmental processes. TGFbeta1 has been localized to mitochondria in rat liver cells and muscle cells. In the present study, we examined the expression of TGFbeta isoform mRNAs and proteins during chicken embryonic lens development. PCR analysis demonstrated TGFbeta2 and TGFbeta3 transcripts in the lens epithelium and fibers throughout pre- and post-hatching development. TGFbeta isoforms were detected throughout the lens epithelium and fibers early in development (E6). However by E19, the distribution of TGFbeta2 and TGFbeta3 transcripts and proteins coincided with regions of the lens that contained mitochondria. In addition, intense TGFbeta staining was observed in the basal portions of the equatorial epithelial cells, a region with abundant mitochondria. Transcripts for TGFbeta1 and **TGFbeta4** were not detected in any tissue or time frame examined. Similarly, no immunostaining for TGFbeta1 was observed.

DRUG DESCRIPTORS:
*transforming growth factor beta
MEDICAL DESCRIPTORS:
*embryo development; *gene expression; *lens
animal cell; article; cell differentiation; cell maturation; cell organelle ; chick embryo; embryo; immunoblotting; immunohistochemistry; lens epithelium; mitochondrion; nonhuman; polymerase chain reaction; priority journal
SECTION HEADINGS:
021 Developmental Biology and Teratology

**Cloning and characterization of human polyamine-modulated factor-1, a transcriptional cofactor that regulates the transcription of the spermidine/spermine N(1)-acetyltransferase gene.**

Wang Y; Devereux W; Stewart T M; Casero R A

Johns Hopkins Oncology Center Research Laboratories, Baltimore, Maryland 21231, USA.

Journal of biological chemistry (UNITED STATES) Jul 30 1999, 274 (31) p22095-101, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: CA51085; CA; NCI; CA58184; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The increased transcription and ultimate superinduction of the spermidine/spermine N(1)-acetyltransferase (SSAT) gene has been associated with the antineoplastic activity of several new antitumor polyamine analogues. In sensitive tumor cell types, the transcriptional induction appears to be regulated by the constitutive association of the transcription factor Nrf-2 with the recently discovered polyamine-responsive element. Using the yeast two-hybrid system, a new transcriptional cofactor, polyamine-modulated factor-1 (PMF-1), has been identified as a partner protein of Nrf-2 that, in combination with Nrf-2, regulates the polyamine analogue-induced transcription of SSAT. The human **PMF - 1 gene**, located on chromosome **1** near the 1q12/1q21 border, yields an mRNA transcript of approximately 1.2 kilobases that codes for a 165-amino acid protein with a predicted molecular mass of approximately 20 kDa. The PMF-1 mRNA appears to increase in response to analogue exposure only in analogue-responsive cells. In addition to the transcriptional regulation of SSAT, PMF-1 or similar factors should be considered in the regulation of other polyamine-dependent genes.

Tags: Female; Human; Pregnancy; Support, U.S. Gov't, P.H.S.

Descriptors: *Acetyltransferases--genetics--GE; *Chromosomes, Human, Pair 1; *Gene Expression Regulation, Enzymologic; *Transcription Factors --genetics--GE; *Transcription Factors--metabolism--ME; *Transcription, Genetic; Amino Acid Sequence; Base Sequence; Cell Line; Chromosome Mapping; Cloning, Molecular; DNA Primers; DNA-Binding Proteins--metabolism--ME; Exons; Gene Library; Introns; Molecular Sequence Data; Molecular Weight; Placenta--metabolism--ME; RNA, Messenger--genetics--GE; Recombinant Proteins--chemistry--CH; Transcription Factors--chemistry--CH; Transfection

Molecular Sequence Databank No.: GENBANK/AF141308; GENBANK/AF141309; GENBANK/AF141310; GENBANK/AH008078

CAS Registry No.: 0 (DNA Primers); 0 (DNA-Binding Proteins); 0 (RNA, Messenger); 0 (Recombinant Proteins); 0 (Transcription Factors); 0 (nuclear respiratory factor 2); 0 (polyamine-modulated factor 1)

Enzyme No.: EC 2.3.1. (Acetyltransferases); EC 2.3.1.57 (spermidine acetyltransferase)

Record Date Created: 19990819

Record Date Completed: 19990819